

Sequence Listing

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (ii) TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
- (iii) NUMBER OF SEQUENCES: 131
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Genentech, Inc.
 - (B) STREET: 1 DNA Way
 - (C) CITY: South San Francisco
 - (D) STATE: California
 - (E) COUNTRY: USA
 - (F) ZIP: 94080

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: WinPatin (Genentech)

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: 09/723752
- (B) FILING DATE: 27-Nov-2000
- (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 08/908469
- (B) FILING DATE: 06-AUG-1997

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 08/833504
- (B) FILING DATE: 07-APR-1997

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Cui, Steven X.
- (B) REGISTRATION NUMBER: 44,637
- (C) REFERENCE/DOCKET NUMBER: P1093P1D1

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 650/225-8674
- (B) TELEFAX: 650/952-9881

(2) INFORMATION FOR SEQ ID NO:1:
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 10 amino acids(B) TYPE: Amino Acid(D) TOPOLOGY: Linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
Gly Tyr Thr Phe Thr Asn Tyr Gly Met Asn 1 5 10
(2) INFORMATION FOR SEQ ID NO:2:
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 17 amino acids(B) TYPE: Amino Acid(D) TOPOLOGY: Linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Ala Asp Phe 1 5 10 15
Lys Arg
(2) INFORMATION FOR SEQ ID NO:3:
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 14 amino acids(B) TYPE: Amino Acid(D) TOPOLOGY: Linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
Tyr Pro His Tyr Tyr Gly Ser Ser His Trp Tyr Phe Asp Val
(2) INFORMATION FOR SEQ ID NO:4:
(2) INFORMATION FOR SEQ ID NO:4: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 11 amino acids (B) TYPE: Amino Acid (D) TOPOLOGY: Linear
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 11 amino acids (B) TYPE: Amino Acid

(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 7 amino acids(B) TYPE: Amino Acid(D) TOPOLOGY: Linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:	
Phe Thr Ser Ser Leu His Ser 1 5	
(2) INFORMATION FOR SEQ ID NO:6:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 9 amino acids(B) TYPE: Amino Acid(D) TOPOLOGY: Linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:	
Gln Gln Tyr Ser Thr Val Pro Trp Thr 1 5	
/a\	
(2) INFORMATION FOR SEQ ID NO:7:	
(2) INFORMATION FOR SEQ ID NO:7: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 118 amino acids (B) TYPE: Amino Acid (D) TOPOLOGY: Linear	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 118 amino acids (B) TYPE: Amino Acid	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 118 amino acids(B) TYPE: Amino Acid(D) TOPOLOGY: Linear	Gly 15
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 118 amino acids (B) TYPE: Amino Acid (D) TOPOLOGY: Linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7: Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro	15
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 118 amino acids (B) TYPE: Amino Acid (D) TOPOLOGY: Linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7: Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro- 1 5 10 Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Thr Phe	15 Thr 30
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 118 amino acids (B) TYPE: Amino Acid (D) TOPOLOGY: Linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7: Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro- 1 5 10 Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Thr Phe 20 25 Asn Tyr Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly	15 Thr 30 Leu 45
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 118 amino acids (B) TYPE: Amino Acid (D) TOPOLOGY: Linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7: Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro- 1 5 10 Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Thr Phe 20 25 Asn Tyr Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly 35 40 Glu Trp Val Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr	15 Thr 30 Leu 45 Tyr 60

(2) INFORMATION FOR SEQ ID NO:5:

Thr Ala	Val Tyr	Tyr C ₎ 95	rs Ala	Lys	Tyr	Pro 100	His	Tyr	Tyr	Gly	Ser 105
Ser His	Trp Tyr	Phe As	sp Val	Trp	Gly	Gln 115	Gly	Thr	Leu		
(2) INFOR	MATION E	OR SEC	ID N	0:8:							
(A (B	-	H: 110 Amino	amino Acid		ds						
(xi) SE	QUENCE I	DESCRIE	TION:	SEQ	ID 1	10:8	:				
Asp Ile (Gln Met	Thr Gl	n Ser	Pro	Ser	Ser 10	Leu	Ser	Ala	Ser	Val 15
Gly Asp	Arg Val	Thr Il	e Thr	Cys	Ser	Ala 25	Ser	Gln	Asp	Ile	Ser 30
Asn Tyr	Leu Asn	Trp Ty 35	r Gln	Gln	Lys	Pro 40	Gly	Lys	Ala	Pro	Lys 45
Val Leu	Ile Tyr	Phe Th	r Ser	Ser	Leu	His 55	Ser	Gly	Val	Pro	Ser 60
Arg Phe	Ser Gly	Ser Gl 65	y Ser	Gly	Thr	Asp 70	Phe	Thr	Leu	Thr	Ile 75
Ser Ser I	Leu Gln	Pro Gl 80	u Asp	Phe	Ala	Thr 85	Tyr	Tyr	Cys	Gln	Gln 90
Tyr Ser	Thr Val	Pro Tr 95	p Thr	Phe	Gly	Gln 100	Gly	Thr	Lys	Val	Glu 105
Ile Lys A	Arg Thr	Val 110									
(2) INFOR	MATION F	OR SEC	ID NO	0:9:							
(A)	QUENCE C LENGTH TYPE: TOPOLC	I: 123 Amino	amino Acid		ls						
(xi) SE	QUENCE D	ESCRIP	TION:	SEQ	ID N	10 : 9 :					
Glu Ile (Gln Leu	Val Gl 5	n Ser	Gly	Pro	Glu 10	Leu	Lys	Gln	Pro	Gly 15

Glu	Thr	Val	Arg	Ile 20	Ser	Cys	Lys	Ala	Ser 25	Gly	Tyr	Thr	Phe	Thr 30
Asn	Tyr	Gly	Met	Asn 35	Trp	Val	Lys	Gln	Ala 40	Pro	Gly	Lys	Gly	Leu 45
Lys	Trp	Met	Gly	Trp 50	Ile	Asn	Thr	Tyr	Thr 55	Gly	Glu	Pro	Thr	Tyr 60
Ala	Ala	Asp	Phe	Lys 65	Arg	Arg	Phe	Thr	Phe 70	Ser	Leu	Glu	Thr	Ser 75
Ala	Ser	Thr	Ala	Tyr 80	Leu	Gln	Ile	Ser	Asn 85	Leu	Lys	Asn	Asp	Asp 90
Thr	Ala	Thr	Tyr	Phe 95	Cys	Ala	Lys	Tyr	Pro 100	His	Tyr	Tyr	Gly	Ser 105
Ser	His	Trp	Tyr	Phe 110	Asp	Val	Trp	Gly	Ala 115	Gly	Thr	Thr	Val	Thr 120
Val	Ser	Ser												
(2)	INFO	RMAT]	ON E	OR S	SEO I	ID NO	0:10:							
	(<i>1</i>	EQUEN	NCE (ENGTH (PE:	CHARA I: 10 Amir	ACTER 08 an	RISTI mino cid	CS:	_						
(:	(EQUEN A) LI B) TY	NCE (ENGTH (PE:	CHARA I: 10 Amir OGY:	ACTER 08 an 10 Ac Line	RISTI mino cid ear	CS: acio	ls	IO:10):				
(i	(<i>I</i> (I (I	EQUEN A) LI B) TY C) TO	NCE (ENGTH (PE:	CHARA H: 10 Amir OGY:	ACTER 08 and 10 Ac Line	RISTI mino cid ear	(CS: acid	is			Ser	Ala	Ser	Leu 15
(xi	(A (F (I (I) SI	EQUEN A) LI B) TY C) TO EQUEN	NCE (ENGTH (PE: OPOLO	CHARA H: 10 Amir OGY: DESCR Thr	ACTER 08 and 10 Ac Line RIPT1	RISTI nino cid ear ION:	(CS: acio SEQ Thr	ds ID N Ser	Ser 10	Leu				15
(xi	(1 (I (I i) SI Ile	EQUEN A) LI B) TY D) TO EQUEN Gln	NCE (ENGTH (PE:)POLO NCE I	CHARA H: 10 Amir OGY: DESCR Thr 5 Ile 20	ACTER 08 an 10 Ac Line RIPTI Gln	RISTIMINO cid ear ION:	CCS: acid SEQ Thr	lb N Ser Ser	Ser 10 Ala 25	Leu Ser	Gln	Asp	Ile	15 Ser 30
(xi 'Asp 1 Gly Asn	(1) (Iii) SH	EQUEN A) LH B) TY D) TO EQUEN Gln Arg	NCE (ENGTH (PE: DPOLC NCE I Met	CHARA H: 10 Amir DGY: DESCR Thr 5 Ile 20 Trp 35	ACTER 08 an no Ac Line RIPT) Gln Ile	RISTIMINO cid ear CON: Thr	CCS: acid SEQ Thr Cys	is ID N Ser Ser Lys	Ser 10 Ala 25 Pro 40	Leu Ser Asp	Gln Gly	Asp Thr	Ile Val	15 Ser 30 Lys 45
(xiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiii	(1) (Iii) SIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	EQUENCY TO	NCE (ENGTH (PE: DPOLO NCE I Met Val	CHARA H: 10 Amir OGY: DESCR Thr 5 Ile 20 Trp 35 Phe 50	ACTER 08 an 10 Ac Line RIPTI Gln Ile Tyr Thr	RISTIMINO CID CONTROL	SEQ Thr Cys Gln	ID N Ser Ser Lys Leu	Ser 10 Ala 25 Pro 40 His 55	Leu Ser Asp	Gln Gly Gly	Asp Thr Val	Ile Val Pro	15 Ser 30 Lys 45 Ser 60

(2) INFORMA	rion for	SEQ ID N	0:11	:						
(A) 1 (B) 5	ENCE CHAR LENGTH: 1 FYPE: Ami FOPOLOGY:	13 amino no Acid		ds						
(xi) SEQUI	ENCE DESC	RIPTION:	SEQ	ID I	NO:1	1:				
Glu Val Gli 1	n Leu Val 5	Glu Ser	Gly	Gly	Gly 10	Leu	Val	Gln	Pro	Gly 15
Gly Ser Le	ı Arg Leu 20	Ser Cys	Ala	Ala	Ser 25	Gly	Phe	Thr	Phe	Ser 30
Ser Tyr Ala	a Met Ser 35	Trp Val	Arg	Gln	Ala 40	Pro	Gly	Lys	Gly	Leu 45
Glu Trp Val	l Ser Val 50	Ile Ser	Gly	Asp	Gly 55	Gly	Ser	Thr	Tyr	Tyr 60
Ala Asp Ser	r Val Lys 65	Gly Arg	Phe	Thr	Ile 70	Ser	Arg	Asp	Asn	Ser 75
Lys Asn Thi	r Leu Tyr 80	Leu Gln	Met	Asn	Ser 85	Leu	Arg	Ala	Glu	Asp 90
Thr Ala Val	l Tyr Tyr 95	Cys Ala	Arg	Gly	Phe 100	Asp	Tyr	Trp	Gly	Gln 105
Gly Thr Lev	ı Val Thr 110	Val Ser	Ser							
(2) INFORMAT	TION FOR	SEQ ID N	0:12:	:						
(A) I (B) 7	ENCE CHAR LENGTH: 1 TYPE: Ami TOPOLOGY:	08 amino no Acid		ls						
(xi) SEQUE	ENCE DESC	RIPTION:	SEQ	ID N	10:12	2:				
Asp Ile Glr 1	n Met Thr 5	Gln Ser	Pro	Ser	Ser 10	Leu	Ser	Ala	Ser	Val 15

Tyr Ser Thr Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu

Ile Lys Arg

100

Gly	Asp	Arg	Val	Thr 20	Ile	Thr	Cys	Arg	Ala 25	Ser	Gln	Ser	Ile	Ser 30
Asn	Tyr	Leu	Ala	Trp 35	Tyr	Gln	Gln	Lys	Pro 40	Gly	Lys	Ala	Pro	Lys 45
Leu	Leu	Ile	Tyr	Ala 50	Ala	Ser	Ser	Leu	Glu 55	Ser	Gly	Val	Pro	Ser 60
Arg	Phe	Ser	Gly	Ser 65	Gly	Ser	Gly	Thr	Asp 70	Phe	Thr	Leu	Thr	Ile 75
Ser	Ser	Leu	Gln	Pro 80	Glu	Asp	Phe	Ala	Thr 85	Tyr	Tyr	Cys	Gln	Gln 90
Tyr	Asn	Ser	Leu	Pro 95	Trp	Thr	Phe	Gly	Gln 100	Gly	Thr	Lys	Val	Glu 105
Ile	Lys	Arg												
(2)	INFOI	RMAT	ON E	OR S	SEQ I	D NO	0:13:	:						
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(:	•	~	VCE (ICS: acio	ł.c						
	1.5	T/ 131	714 C T T		,, an	ILTIU	$u \cup v = v$							
	(I	3) TY	PE:	Amir	no Ad	cid	uci	45						
(xi	(I	3) TY O) T(PE:	Amir OGY:	no Ad Line	cid ear			10:1 3	3:				
	(I (I i) SI	B) TY D) TO EQUE	PE:	Amir OGY: DESCI	no Ad Line	cid ear	SEQ	ID 1			Ser	Ala	Ser	Val
Asp 1	(F (I i) SF Ile	3) TY D) TO EQUEN	PE: POLC	Amir OGY: DESCI Thr 5	no Ac Line RIPTI Gln	cid ear ION: Ser	SEQ Pro	ID N	Ser 10	Leu				15
Asp 1 Gly	(I (I i) SI Ile Asp	B) TY C) TO EQUEN Gln Arg	YPE: DPOLO NCE I Met	Amir OGY: DESCE Thr 5 Thr 20	no Ac Line RIPTI Gln Ile	eid ear ION: Ser Thr	SEQ Pro Cys	ID N Ser	Ser 10 Ala 25	Leu Ser	Gln	Asp	Ile	15 Ser 30
Asp 1 Gly Asn	(I (I Ile Asp	B) TY D) TO EQUEN Gln Arg	(PE: DPOLO NCE I Met Val	Amir OGY: DESCE Thr 5 Thr 20 Trp 35	Line RIPTI Gln Ile	eid ear ION: Ser Thr	SEQ Pro Cys Gln	ID N Ser Ser Lys	Ser 10 Ala 25 Pro 40	Leu Ser Gly	Gln Lys	Asp	Ile Pro	15 Ser 30 Lys 45
Asp 1 Gly Asn Leu	(I (I i) SI Ile Asp Tyr	B) TY D) TO EQUEN Gln Arg Leu Ile	(PE: DPOLC NCE I Met Val	Amir DGY: DESCE Thr 5 Thr 20 Trp 35 Phe 50	Line CIPTI Gln Ile Tyr	cid ear ION: Ser Thr Gln Ser	SEQ Pro Cys Gln Ser	ID N Ser Ser Lys	Ser 10 Ala 25 Pro 40 His 55	Leu Ser Gly Ser	Gln Lys Gly	Asp Ala Val	Ile Pro	Ser 30 Lys 45 Ser
Asp 1 Gly Asn Leu	(I (I i) SI Ile Asp Tyr Leu	B) TY D) TO EQUEN Gln Arg Leu Ile Ser	PE: DPOLC NCE I Met Val Asn	Amir OGY: DESCR Thr 5 Thr 20 Trp 35 Phe 50 Ser 65	Line RIPTI Gln Ile Tyr Thr	cid ear ION: Ser Thr Gln Ser Ser	SEQ Pro Cys Gln Ser	ID N Ser Ser Lys Leu	Ser 10 Ala 25 Pro 40 His 55 Asp	Leu Ser Gly Ser	Gln Lys Gly Thr	Asp Ala Val Leu	Ile Pro Pro Thr	15 Ser 30 Lys 45 Ser 60 Ile 75

۲,

Ile Lys

(2)	INFO	RMAT:	ION I	FOR S	SEQ :	ID N	0:14	:						
	(,	-	ENGTI YPE :	H: 12 Amir	23 at	mino cid		ds						
()	ci) S	EQUEI	NCE I	DESCI	RIPT	ION:	SEQ	ID I	NO:14	4:				
Glu	ı Val	Gln	Leu	Val 5	Glu	Ser	Gly	Gly	Gly 10	Leu	Val	Gln	Pro	Gl;
Gly	/ Ser	Leu	Arg	Leu 20	Ser	Cys	Ala	Ala	Ser 25	Gly	Tyr	Thr	Phe	Th:
Asr	ı Tyr	Gly	Met	Asn 35	Trp	Val	Arg	Gln	Ala 40	Pro	Gly	Lys	Gly	Let
Glı	ı Trp	Val	Gly	Trp 50	Ile	Asn	Thr	Tyr	Thr 55	Gly	Glu	Pro	Thr	Ту: 60
Ala	a Ala	Asp	Phe	Lys 65	Arg	Arg	Phe	Thr	Ile 70	Ser	Arg	Asp	Asn	Se:
Lys	s Asn	Thr	Leu	Tyr 80	Leu	Gln	Met	Asn	Ser 85	Leu	Arg	Ala	Glu	Asp 90
Thi	Ala	Val	Tyr	Tyr 95	Cys	Ala	Arg	Tyr	Pro 100	His	Tyr	Tyr	Gly	Se:
Sei	His	Trp	Tyr	Phe	_	Val	Trp	Gly	Gln	-	Thr	Leu	Val	Thi

Val Ser Ser

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 107 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val 1 5 10 15

Gly	Asp	Arg	Val	Thr 20	Ile	Thr	Cys	Ser	Ala 25	Ser	Gln	Asp	Ile	Ser 30
Asn	Tyr	Leu	Asn	Trp 35	Tyr	Gln	Gln	Lys	Pro 40	Gly	Lys	Ala	Pro	Lys 45
Leu	Leu	Ile	Tyr	Phe 50	Thr	Ser	Ser	Leu	His 55	Ser	Gly	Val	Pro	Ser 60
Arg	Phe	Ser	Gly	Ser 65	Gly	Ser	Gly	Thr	Asp 70	Tyr	Thr	Leu	Thr	Ile 75
Ser	Ser	Leu	Gln	Pro 80	Glu	Asp	Phe	Ala	Thr 85	Tyr	Tyr	Cys	Gln	Gln 90
Tyr	Ser	Thr	Val	Pro 95	Trp	Thr	Phe	Gly	Gln 100	Gly	Thr	Lys	Val	Glu 105
Ile	Lys													
(2)	INFO	TAMS	ON E	FOR S	SEQ I	D NO	0:16:	:						
(:	i) SI		ICE (
	/ 1	,)	727CTT		`			-						
	(1	3) TY	ENGTE PE: POLC	Amir	no Ac	cid	ació	ıs						
(x:	(I)	3) TY O) TO	PE:	Amir OGY:	no Ad Line	cid ear			NO:16	5 :				
-	(I (I i) SI	3) TY O) TO EQUEN	PE:	Amir)GY:)ESCF	no Ad Line	eid ear ION:	SEQ	ID 1			Val	Gln	Pro	Gly 15
Glu 1	(I (I i) SI Val	3) TY D) TO EQUEN	PE: POLC	Amir OGY: DESCF Val 5	no Ac Line RIPT:	cid ear ION: Ser	SEQ Gly	ID N	Gly 10	Leu				15
Glu 1 Gly	(H (I i) SH Val Ser	3) TY D) TO EQUEN Gln Leu	(PE: DPOLO NCE I Leu	Amir DGY: DESCF Val 5 Leu 20	no Ad Line RIPTI Glu Ser	cid ear ION: Ser Cys	SEQ Gly Ala	ID N Gly Ala	Gly 10 Ser 25	Leu Gly	Tyr	Thr	Phe	15 Thr 30
Glu 1 Gly Asn	(H (I (I) SH Val Ser	B) TY D) TO EQUEN Gln Leu Gly	(PE: DPOLO NCE I Leu Arg	Amir DESCF Val 5 Leu 20 Asn 35	Line RIPTI Glu Ser	cid ear ION: Ser Cys	SEQ Gly Ala Arg	ID N Gly Ala Gln	Gly 10 Ser 25 Ala 40	Leu Gly Pro	Tyr Gly	Thr Lys	Phe Gly	15 Thr 30 Leu 45
Glu 1 Gly Asn Glu	(I (I i) SI Val Ser Tyr	B) TY D) TO EQUEN Gln Leu Gly Val	(PE: DPOL(NCE I Leu Arg	Amir DGY: DESCF Val 5 Leu 20 Asn 35 Trp 50	Line ClpT Glu Ser Trp	cid ear ION: Ser Cys Ile Asn	SEQ Gly Ala Arg	ID N Gly Ala Gln Tyr	Gly 10 Ser 25 Ala 40 Thr	Leu Gly Pro Gly	Tyr Gly Glu	Thr Lys Pro	Phe Gly Thr	15 Thr 30 Leu 45 Tyr 60
Glu 1 Gly Asn Glu Ala	(H (I (I) SH Val Ser Tyr Trp	B) TY D) TO COURT Gln Leu Gly Val Asp	PE: DPOLO NCE I Leu Arg Met Gly	Amir DESCF Val 5 Leu 20 Asn 35 Trp 50 Lys 65	Line RIPTI Glu Ser Trp Ile Arg	cid ear ION: Ser Cys Ile Asn	SEQ Gly Ala Arg Thr	ID N Gly Ala Gln Tyr	Gly 10 Ser 25 Ala 40 Thr 55 Ile 70	Leu Gly Pro Gly Ser	Tyr Gly Glu Leu	Thr Lys Pro Asp	Phe Gly Thr	15 Thr 30 Leu 45 Tyr 60 Ser 75

Ser His Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Leu Val Thr
110 115 120

Val Ser Ser

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Pro Lys Asn Ser Ser Met Ile Ser Asn Thr Pro 1 5 10

- (2) INFORMATION FOR SEQ ID NO:18:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

His Gln Ser Leu Gly Thr Gln
1 5

- (2) INFORMATION FOR SEQ ID NO:19:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

His Gln Asn Leu Ser Asp Gly Lys
1 5

- (2) INFORMATION FOR SEQ ID NO:20:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

His Gln Asn Ile Ser Asp Gly Lys
1 5

- (2) INFORMATION FOR SEQ ID NO:21:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Val Ile Ser Ser His Leu Gly Gln
1 5

- (2) INFORMATION FOR SEQ ID NO:22:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 66 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GATTTCAAAC GTCGTNYTAC TWTTTCTAGA GACAACTCCA AAAACACABY 50

TTACCTGCAG ATGAAC 66

- (2) INFORMATION FOR SEQ ID NO:23:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 66 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GATTTCAAAC GTCGTNYTAC TWTTTCTTTA GACACCTCCG CAAGCACABY 50

TTACCTGCAG ATGAAC 66

- (2) INFORMATION FOR SEQ ID NO:24:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single

- (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AGCCTGCGCG CTGAGGACAC TGCCGTCTAT TACTGTDYAA RGTACCCCCA 50

CTATTATGGG 60

- (2) INFORMATION FOR SEQ ID NO:25:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CTCAGCGCGC AGGCTGTTCA TCTGCAGGTA 30

- (2) INFORMATION FOR SEQ ID NO:26:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GCTGATATCC AGTTGACCCA GTCCCCG 27

- (2) INFORMATION FOR SEQ ID NO:27:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TCTGGGACGG ATTACACTCT GACCATC 27

- (2) INFORMATION FOR SEQ ID NO:28:
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CGTTTGTCCT GTGCARYTTC TGGCTATACC TTCACCAACT ATGGTATGAA 50

CTGGRTCCGT CAGGCCCCGG GTAAG 75

- (2) INFORMATION FOR SEQ ID NO:29:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GATATCCAGT TGACCCAGTC CCCG 24

- (2) INFORMATION FOR SEQ ID NO:30:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GCTCCGAAAG TACTGATTTA C 21

- (2) INFORMATION FOR SEQ ID NO:31:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 54 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CGTCGTTTCA CTTTTTCTGC AGACACCTCC AGCAACACAG TATACCTGCA 50

GATG 54

- (2) INFORMATION FOR SEQ ID NO:32:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CTATTACTGT GCAAAGTACC CCCAC 25

- (2) INFORMATION FOR SEQ ID NO:33:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GGGACGGATT TCACTCTGAC CATC 24

- (2) INFORMATION FOR SEQ ID NO:34:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GGTATGAACT GGGTCCGTCA GGCCCC 26

- (2) INFORMATION FOR SEQ ID NO:35:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CGTCGTTTCA CTTTTCTTT AGACACCTCC AAAAGCACAG CATACCTGCA 50
GATGAAC 57

- (2) INFORMATION FOR SEQ ID NO:36:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 53 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GGGTCACCAT CACCTGCTAA GCATAATAAT AATAAAGCAA CTATTTAAAC 50
TGG 53

- (2) INFORMATION FOR SEQ ID NO:37:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GCGCAAGTCA GGATATTTAA TAATAATAAT AATGGTATCA ACAGAAACCA 50 GG 52

- (2) INFORMATION FOR SEQ ID NO:38:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GTCTATTACT GTGCAAAGTA ATAACACTAA TAAGGGAGCA GCCACTGG 48

- (2) INFORMATION FOR SEQ ID NO:39:
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GGTACCCCCA CTATTATTAA TAATAATAAT GGTATTTCGA CGTCTGGGG 49

- (2) INFORMATION FOR SEQ ID NO:40:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 53 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CACTATTATG GGAGCAGCCA CTAATAATAA TAAGTCTGGG TCAAGGAACC 50

1

CTG 53

- (2) INFORMATION FOR SEQ ID NO:41:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 53 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

TCCTGTGCAG CTTCTGGCTA ATAATTCTAA TAATAAGGTA TGAACTGGGT 50

CCG 53

- (2) INFORMATION FOR SEQ ID NO:42:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GAATGGGTTG GATGGATTAA CTAATAATAA GGTTAACCGA CCTATGCTGC 50

GG 52

- (2) INFORMATION FOR SEQ ID NO:43:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 49 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CTGTGCAAAG TACCCGTAAT ATTAATAATA ATAACACTGG TATTTCGAC 49

- (2) INFORMATION FOR SEQ ID NO:44:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

CGTTTCACTT TTTCTTAAGA CTAATCCAAA TAAACAGCAT ACCTGCAG 48

- (2) INFORMATION FOR SEQ ID NO:45:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GAATGGGTTG GATGGATTTA ATAATAATAA GGTGAACCGA CCTATG 46

- (2) INFORMATION FOR SEQ ID NO:46:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 53 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GGGTCACCAT CACCTGCNNS GCANNSNNSN NSNNSAGCAA CTATTTAAAC 50

TGG 53

- (2) INFORMATION FOR SEQ ID NO:47:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GCGCAAGTCA GGATATTNNS NNSNNSNNSN NSTGGTATCA ACAGAAACCA 50

GG 52

- (2) INFORMATION FOR SEQ ID NO:48:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GTCTATTACT GTGCAAAGNN SNNSCACNNS NNSGGGAGCA GCCACTGG 48

- (2) INFORMATION FOR SEQ ID NO:49:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 49 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GGTACCCCCA CTATTATNNS NNSNNSNNST GGTATTTCGA CGTCTGGGG 49

- (2) INFORMATION FOR SEQ ID NO:50:
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

CACTATTATG GGAGCAGCCA CNNSNNSNNS NNSGTCTGGG GTCAAGGAAC 50
CCTG 54

- (2) INFORMATION FOR SEQ ID NO:51:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 53 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TCCTGTGCAG CTTCTGGCNN SNNSTTCNNS NNSNNSGGTA TGAACTGGGT 50
CCG 53

- - (i) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO:52:

- (A) LENGTH: 52 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GAATGGGTTG GATGGATTAA CNNSNNSNNS GGTNNSCCGA CCTATGCTGC 50

GG 52

- (2) INFORMATION FOR SEQ ID NO:53:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 49 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CTGTGCAAAG TACCCGNNST ATNNSNNSNN SNNSCACTGG TATTTCGAC 49

- (2) INFORMATION FOR SEQ ID NO:54:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CGTTTCACTT TTTCTNNSGA CNNSTCCAAA NNSACAGCAT ACCTGCAG 48

- (2) INFORMATION FOR SEQ ID NO:55:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GAATGGGTTG GATGGATTNN SNNSNNSNNS GGTGAACCGA CCTATG 46

- (2) INFORMATION FOR SEQ ID NO:56:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Tyr Pro Tyr Tyr Arg Gly Thr Ser His Trp Tyr Phe Asp

1 5 10

- (2) INFORMATION FOR SEQ ID NO:57:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Tyr Pro Tyr Tyr Ile Asn Lys Ser His Trp Tyr Phe Asp 1 5 10

- (2) INFORMATION FOR SEQ ID NO:58:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Tyr Pro Tyr Tyr Tyr Gly Thr Ser His Trp Tyr Phe Asp 1 5 10

- (2) INFORMATION FOR SEQ ID NO:59:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Tyr Pro Tyr Tyr Tyr Asn Gln Ser His Trp Tyr Phe Asp

1 10

- (2) INFORMATION FOR SEQ ID NO:60:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Tyr Pro Tyr Tyr Ile Ala Lys Ser His Trp Tyr Phe Asp 1 5 10

- (2) INFORMATION FOR SEQ ID NO:61:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Tyr Pro Tyr Tyr Arg Asp Asn Ser His Trp Tyr Phe Asp

1 10

- (2) INFORMATION FOR SEQ ID NO:62:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Tyr Pro Tyr Tyr Trp Gly Thr Ser His Trp Tyr Phe Asp

- (2) INFORMATION FOR SEQ ID NO:63:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Tyr Pro Tyr Tyr Arg Gln Asn Ser His Trp Tyr Phe Asp

- (2) INFORMATION FOR SEQ ID NO:64:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Tyr Pro Tyr Tyr Arg Gln Ser Ser His Trp Tyr Phe Asp
1 5 10

- (2) INFORMATION FOR SEQ ID NO:65:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Tyr Pro Tyr Tyr Arg Asn Thr Ser His Trp Tyr Phe Asp
1 5 10

- (2) INFORMATION FOR SEQ ID NO:66:
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Tyr Pro Tyr Tyr Lys Asn Thr Ser His Trp Tyr Phe Asp
1 5 10

- (2) INFORMATION FOR SEQ ID NO:67:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Tyr Pro Tyr Tyr Ile Glu Arg Ser His Trp Tyr Phe Asp 1 5 10

- (2) INFORMATION FOR SEQ ID NO:68:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Tyr Pro Tyr Tyr Arg Asn Ala Ser His Trp Tyr Phe Asp
1 5 10

- (2) INFORMATION FOR SEQ ID NO:69:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Tyr Pro Tyr Tyr Thr Thr Arg Ser His Trp Tyr Phe Asp
1 5 10

- (2) INFORMATION FOR SEQ ID NO:70:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:
- Tyr Pro Tyr Tyr Glu Gly Ser Ser His Trp Tyr Phe Asp
 1 5 10
- (2) INFORMATION FOR SEQ ID NO:71:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Tyr Pro Tyr Tyr Arg Gln Arg Gly His Trp Tyr Phe Asp 1 5 10

- (2) INFORMATION FOR SEQ ID NO:72:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Tyr Pro Tyr Tyr Thr Gly Arg Ser His Trp Tyr Phe Asp
1 5 10

- (2) INFORMATION FOR SEQ ID NO:73:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Tyr Pro Tyr Tyr Thr Asn Thr Ser His Trp Tyr Phe Asp

1 5 10

- (2) INFORMATION FOR SEQ ID NO:74:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Tyr Pro Tyr Tyr Arg Lys Gly Ser His Trp Tyr Phe Asp
1 5 10

- (2) INFORMATION FOR SEQ ID NO:75:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Tyr Pro Tyr Tyr Thr Gly Ser Ser His Trp Tyr Phe Asp
1 5 10

- (2) INFORMATION FOR SEQ ID NO:76:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Tyr Pro Tyr Tyr Arg Ser Gly Ser His Trp Tyr Phe Asp 1 5 10

- (2) INFORMATION FOR SEQ ID NO:77:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Tyr Pro Tyr Tyr Thr Asn Arg Ser His Trp Tyr Phe Asp
1 5 10

- (2) INFORMATION FOR SEQ ID NO:78:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Tyr Pro Tyr Tyr Arg Asn Ser Ser His Trp Tyr Phe Asp

1 5 10

- (2) INFORMATION FOR SEQ ID NO:79:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Tyr Pro Tyr Tyr Lys Glu Ser Ser His Trp Tyr Phe Asp
1 10

- (2) INFORMATION FOR SEQ ID NO:80:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Tyr Pro Tyr Tyr Arg Asp Ala Ser His Trp Tyr Phe Asp
1 5 10

- (2) INFORMATION FOR SEQ ID NO:81:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Tyr Pro Tyr Tyr Arg Gln Lys Gly His Trp Tyr Phe Asp
1 5 10

- (2) INFORMATION FOR SEQ ID NO:82:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Tyr Pro Tyr Tyr Lys Gly Gly Ser His Trp Tyr Phe Asp 1 5 10

- (2) INFORMATION FOR SEQ ID NO:83:
 - (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids(B) TYPE: Amino Acid(D) TOPOLOGY: Linear(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Tyr Pro Tyr Tyr Gly Ala Ser His Trp Tyr Phe Asp

- (2) INFORMATION FOR SEQ ID NO:84:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Tyr Pro Tyr Tyr Arg Gly Glu Ser His Trp Tyr Phe Asp

- (2) INFORMATION FOR SEQ ID NO:85:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Tyr Pro Tyr Tyr Arg Ser Thr Ser His Trp Tyr Phe Asp 1 5 10

- (2) INFORMATION FOR SEQ ID NO:86:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Gly Tyr Asp Phe Thr His Tyr Gly Met Asn 1 5 10

- (2) INFORMATION FOR SEQ ID NO:87:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87
Gly Tyr Glu Phe Gln His Tyr Gly Met Asn 1 5 10
(2) INFORMATION FOR SEQ ID NO:88:
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 10 amino acids(B) TYPE: Amino Acid(D) TOPOLOGY: Linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:
Gly Tyr Glu Phe Thr His Tyr Gly Met Asn 1 5 10
(2) INFORMATION FOR SEQ ID NO:89:
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 10 amino acids(B) TYPE: Amino Acid(D) TOPOLOGY: Linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:
Gly Tyr Asp Phe Gly His Tyr Gly Met Asn 1 5 10
(2) INFORMATION FOR SEQ ID NO:90:
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 10 amino acids(B) TYPE: Amino Acid(D) TOPOLOGY: Linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:
Gly Tyr Asp Phe Ser His Tyr Gly Met Asn 1 5 10
(2) INFORMATION FOR SEQ ID NO:91:
(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

(B) TYPE: Amino Acid(D) TOPOLOGY: Linear

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(2) INTOINMITON FOR DBQ ID NO. 32.
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 10 amino acids(B) TYPE: Amino Acid(D) TOPOLOGY: Linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:
Phe Ser Val Asp Val Ser Lys Ser Thr Ala 1 5 10
(2) INFORMATION FOR SEQ ID NO:93:
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 10 amino acids(B) TYPE: Amino Acid(D) TOPOLOGY: Linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:
Phe Ser Leu Asp Lys Ser Lys Ser Thr Ala 1 5 10
(2) INFORMATION FOR SEQ ID NO:94:
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 10 amino acids(B) TYPE: Amino Acid(D) TOPOLOGY: Linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:
Phe Ser Leu Asp Val Trp Lys Ser Thr Ala 1 5 10
(2) INFORMATION FOR SEQ ID NO:95:
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 10 amino acids(B) TYPE: Amino Acid(D) TOPOLOGY: Linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:
Phe Ser Ile Asp Lys Ser Lys Ser Thr Ala 1 5 10

Gly Tyr Glu Phe Ser His Tyr Gly Met Asn

(2) INFORMATION FOR SEQ ID NO:92:

- (2) INFORMATION FOR SEQ ID NO:96:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GCAAAGTACC CGTACTATTA TGGGACGAGC CACTGGTATT TC 42

- (2) INFORMATION FOR SEQ ID NO:97:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

GTCACCATCA CCTGCAGCGC AAGTCAGGAT ATTAGCAACT ATTTAAAC 48

- (2) INFORMATION FOR SEQ ID NO:98:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

CCGTACTATT ATGGGAGCAG CCACTGGTAT TTC 33

- (2) INFORMATION FOR SEQ ID NO:99:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6072 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GAATTCAACT TCTCCATACT TTGGATAAGG AAATACAGAC ATGAAAAATC 50

TCATTGCTGA GTTGTTATTT AAGCTTTGGA GATTATCGTC ACTGCAATGC 100 TTCGCAATAT GGCGCAAAAT GACCAACAGC GGTTGATTGA TCAGGTAGAG 150 GGGGCGCTGT ACGAGGTAAA GCCCGATGCC AGCATTCCTG ACGACGATAC 200 GGAGCTGCTG CGCGATTACG TAAAGAAGTT ATTGAAGCAT CCTCGTCAGT 250 AAAAAGTTAA TCTTTTCAAC AGCTGTCATA AAGTTGTCAC GGCCGAGACT 300 TATAGTCGCT TTGTTTTAT TTTTTAATGT ATTTGTAACT AGAATTCGAG 350 CTCGGTACCC GGGGATCCTC TAGAGGTTGA GGTGATTTTA TGAAAAAGAA 400 TATCGCATTT CTTCTTGCAT CTATGTTCGT TTTTTCTATT GCTACAAACG 450 CGTACGCTGA TATCCAGTTG ACCCAGTCCC CGAGCTCCCT GTCCGCCTCT 500 GTGGGCGATA GGGTCACCAT CACCTGCAGC GCAAGTCAGG ATATTAGCAA 550 CTATTTAAAC TGGTATCAAC AGAAACCAGG AAAAGCTCCG AAACTACTGA 600 TTTACTTCAC CTCCTCTCC CACTCTGGAG TCCCTTCTCG CTTCTCTGGA 650 TCCGGTTCTG GGACGGATTA CACTCTGACC ATCAGCAGTC TGCAGCCAGA 700 AGACTTCGCA ACTTATTACT GTCAACAGTA TAGCACCGTG CCGTGGACGT 750 TTGGACAGGG TACCAAGGTG GAGATCAAAC GAACTGTGGC TGCACCATCT 800 GTCTTCATCT TCCCGCCATC TGATGAGCAG TTGAAATCTG GAACTGCTTC 850 TGTTGTGTGC CTGCTGAATA ACTTCTATCC CAGAGAGGCC AAAGTACAGT 900 GGAAGGTGGA TAACGCCCTC CAATCGGGTA ACTCCCAGGA GAGTGTCACA 950 GAGCAGGACA GCAAGGACAG CACCTACAGC CTCAGCAGCA CCCTGACGCT 1000 GAGCAAAGCA GACTACGAGA AACACAAAGT CTACGCCTGC GAAGTCACCC 1050 ATCAGGGCCT GAGCTCGCCC GTCACAAAGA GCTTCAACAG GGGAGAGTGT 1100 TAAGCTGATC CTCTACGCCG GACGCATCGT GGCCCTAGTA CGCAACTAGT 1150 CGTAAAAAGG GTATCTAGAG GTTGAGGTGA TTTTATGAAA AAGAATATCG 1200 CATTTCTTCT TGCATCTATG TTCGTTTTTT CTATTGCTAC AAACGCGTAC 1250 GCTGAGGTTC AGCTGGTGGA GTCTGGCGGT GGCCTGGTGC AGCCAGGGGG 1300

CTCACTCCGT TTGTCCTGTG CAGCTTCTGG CTATACCTTC ACCAACTATG 1350 GTATGAACTG GATCCGTCAG GCCCCGGGTA AGGGCCTGGA ATGGGTTGGA 1400 TGGATTAACA CCTATACCGG TGAACCGACC TATGCTGCGG ATTTCAAACG 1450 TCGTTTTACT ATATCTGCAG ACACCTCCAG CAACACAGTT TACCTGCAGA 1500 TGAACAGCCT GCGCGCTGAG GACACTGCCG TCTATTACTG TGCAAAGTAC 1550 CCGCACTATT ATGGGAGCAG CCACTGGTAT TTCGACGTCT GGGGTCAAGG 1600 AACCCTGGTC ACCGTCTCCT CGGCCTCCAC CAAGGGCCCA TCGGTCTTCC 1650 CCCTGGCACC CTCCTCCAAG AGCACCTCTG GGGGCACAGC GGCCCTGGGC 1700 TGCCTGGTCA AGGACTACTT CCCCGAACCG GTGACGGTGT CGTGGAACTC 1750 AGGCGCCTG ACCAGCGGCG TGCACACCTT CCCGGCTGTC CTACAGTCCT 1800 CAGGACTCTA CTCCCTCAGC AGCGTGGTGA CCGTGCCCTC CAGCAGCTTG 1850 GGCACCCAGA CCTACATCTG CAACGTGAAT CACAAGCCCA GCAACACCAA 1900 GGTCGACAAG AAAGTTGAGC CCAAATCTTG TGACAAAACT CACCTCTAGA 1950 GTGGCGGTGG CTCTGGTTCC GGTGATTTTG ATTATGAAAA GATGGCAAAC 2000 GCTAATAAGG GGGCTATGAC CGAAAATGCC GATGAAAACG CGCTACAGTC 2050 TGACGCTAAA GGCAAACTTG ATTCTGTCGC TACTGATTAC GGTGCTGCTA 2100 TCGATGGTTT CATTGGTGAC GTTTCCGGCC TTGCTAATGG TAATGGTGCT 2150 ACTGGTGATT TTGCTGGCTC TAATTCCCAA ATGGCTCAAG TCGGTGACGG 2200 TGATAATTCA CCTTTAATGA ATAATTTCCG TCAATATTTA CCTTCCCTCC 2250 CTCAATCGGT TGAATGTCGC CCTTTTGTCT TTAGCGCTGG TAAACCATAT 2300 GAATTTTCTA TTGATTGTGA CAAAATAAAC TTATTCCGTG GTGTCTTTGC 2350 GTTTCTTTA TATGTTGCCA CCTTTATGTA TGTATTTTCT ACGTTTGCTA 2400 ACATACTGCG TAATAAGGAG TCTTAATCAT GCCAGTTCTT TTGGCTAGCG 2450 CCGCCCTATA CCTTGTCTGC CTCCCCGCGT TGCGTCGCGG TGCATGGAGC 2500 CGGGCCACCT CGACCTGAAT GGAAGCCGGC GGCACCTCGC TAACGGATTC 2550 ACCACTCCAA GAATTGGAGC CAATCAATTC TTGCGGAGAA CTGTGAATGC 2600

GCAAACCAAC CCTTGGCAGA ACATATCCAT CGCGTCCGCC ATCTCCAGCA 2650 GCCGCACGCG GCGCATCTCG GGCAGCGTTG GGTCCTGGCC ACGGGTGCGC 2700 ATGATCGTGC TCCTGTCGTT GAGGACCCGG CTAGGCTGGC GGGGTTGCCT 2750 TACTGGTTAG CAGAATGAAT CACCGATACG CGAGCGAACG TGAAGCGACT 2800 GCTGCTGCAA AACGTCTGCG ACCTGAGCAA CAACATGAAT GGTCTTCGGT 2850 TTCCGTGTTT CGTAAAGTCT GGAAACGCGG AAGTCAGCGC CCTGCACCAT 2900 TATGTTCCGG ATCTGCATCG CAGGATGCTG CTGGCTACCC TGTGGAACAC 2950 CTACATCTGT ATTAACGAAG CGCTGGCATT GACCCTGAGT GATTTTTCTC 3000 TGGTCCCGCC GCATCCATAC CGCCAGTTGT TTACCCTCAC AACGTTCCAG 3050 TAACCGGGCA TGTTCATCAT CAGTAACCCG TATCGTGAGC ATCCTCTCTC 3100 GTTTCATCGG TATCATTACC CCCATGAACA GAAATTCCCC CTTACACGGA 3150 GGCATCAAGT GACCAAACAG GAAAAAACCG CCCTTAACAT GGCCCGCTTT 3200 ATCAGAAGCC AGACATTAAC GCTTCTGGAG AAACTCAACG AGCTGGACGC 3250 GGATGAACAG GCAGACATCT GTGAATCGCT TCACGACCAC GCTGATGAGC 3300 TTTACCGCAG GATCCGGAAA TTGTAAACGT TAATATTTTG TTAAAATTCG 3350 CGTTAAATTT TTGTTAAATC AGCTCATTTT TTAACCAATA GGCCGAAATC 3400 GGCAAAATCC CTTATAAATC AAAAGAATAG ACCGAGATAG GGTTGAGTGT 3450 TGTTCCAGTT TGGAACAAGA GTCCACTATT AAAGAACGTG GACTCCAACG 3500 TCAAAGGGCG AAAAACCGTC TATCAGGGCT ATGGCCCACT ACGTGAACCA 3550 TCACCCTAAT CAAGTTTTTT GGGGTCGAGG TGCCGTAAAG CACTAAATCG 3600 GAACCCTAAA GGGAGCCCCC GATTTAGAGC TTGACGGGGA AAGCCGGCGA 3650 ACGTGGCGAG AAAGGAAGGG AAGAAAGCGA AAGGAGCGGG CGCTAGGGCG 3700 CTGGCAAGTG TAGCGGTCAC GCTGCGCGTA ACCACCACAC CCGCCGCGCT 3750 TAATGCGCCG CTACAGGGCG CGTCCGGATC CTGCCTCGCG CGTTTCGGTG 3800 ATGACGGTGA AAACCTCTGA CACATGCAGC TCCCGGAGAC GGTCACAGCT 3850

TGTCTGTAAG CGGATGCCGG GAGCAGACAA GCCCGTCAGG GCGCGTCAGC 3900 GGGTGTTGGC GGGTGTCGGG GCGCAGCCAT GACCCAGTCA CGTAGCGATA 3950 GCGGAGTGTA TACTGGCTTA ACTATGCGGC ATCAGAGCAG ATTGTACTGA 4000 GAGTGCACCA TATGCGGTGT GAAATACCGC ACAGATGCGT AAGGAGAAAA 4050 TACCGCATCA GGCGCTCTTC CGCTTCCTCG CTCACTGACT CGCTGCGCTC 4100 GGTCGTTCGG CTGCGGCGAG CGGTATCAGC TCACTCAAAG GCGGTAATAC 4150 GGTTATCCAC AGAATCAGGG GATAACGCAG GAAAGAACAT GTGAGCAAAA 4200 GGCCAGCAAA AGGCCAGGAA CCGTAAAAAG GCCGCGTTGC TGGCGTTTTT 4250 CCATAGGCTC CGCCCCCTG ACGAGCATCA CAAAAATCGA CGCTCAAGTC 4300 AGAGGTGGCG AAACCCGACA GGACTATAAA GATACCAGGC GTTTCCCCCT 4350 GGAAGCTCCC TCGTGCGCTC TCCTGTTCCG ACCCTGCCGC TTACCGGATA 4400 CCTGTCCGCC TTTCTCCCTT CGGGAAGCGT GGCGCTTTCT CATAGCTCAC 4450 GCTGTAGGTA TCTCAGTTCG GTGTAGGTCG TTCGCTCCAA GCTGGGCTGT 4500 GTGCACGAC CCCCGTTCA GCCCGACCGC TGCGCCTTAT CCGGTAACTA 4550 TCGTCTTGAG TCCAACCCGG TAAGACACGA CTTATCGCCA CTGGCAGCAG 4600 CCACTGGTAA CAGGATTAGC AGAGCGAGGT ATGTAGGCGG TGCTACAGAG 4650 TTCTTGAAGT GGTGGCCTAA CTACGGCTAC ACTAGAAGGA CAGTATTTGG 4700 TATCTGCGCT CTGCTGAAGC CAGTTACCTT CGGAAAAAGA GTTGGTAGCT 4750 CTTGATCCGG CAAACAACC ACCGCTGGTA GCGGTGGTTT TTTTGTTTGC 4800 AAGCAGCAGA TTACGCGCAG AAAAAAAGGA TCTCAAGAAG ATCCTTTGAT 4850 CTTTTCTACG GGGTCTGACG CTCAGTGGAA CGAAAACTCA CGTTAAGGGA 4900 TTTTGGTCAT GAGATTATCA AAAAGGATCT TCACCTAGAT CCTTTTAAAT 4950 TAAAAATGAA GTTTTAAATC AATCTAAAGT ATATATGAGT AAACTTGGTC 5000 TGACAGTTAC CAATGCTTAA TCAGTGAGGC ACCTATCTCA GCGATCTGTC 5050 TATTTCGTTC ATCCATAGTT GCCTGACTCC CCGTCGTGTA GATAACTACG 5100 ATACGGGAGG GCTTACCATC TGGCCCCAGT GCTGCAATGA TACCGCGAGA 5150

CCCACGCTCA CCGGCTCCAG ATTTATCAGC AATAAACCAG CCAGCCGGAA 5200 GGGCCGAGCG CAGAAGTGGT CCTGCAACTT TATCCGCCTC CATCCAGTCT 5250 ATTAATTGTT GCCGGGAAGC TAGAGTAAGT AGTTCGCCAG TTAATAGTTT 5300 GCGCAACGTT GTTGCCATTG CTGCAGGCAT CGTGGTGTCA CGCTCGTCGT 5350 TTGGTATGGC TTCATTCAGC TCCGGTTCCC AACGATCAAG GCGAGTTACA 5400 TGATCCCCCA TGTTGTGCAA AAAAGCGGTT AGCTCCTTCG GTCCTCCGAT 5450 CGTTGTCAGA AGTAAGTTGG CCGCAGTGTT ATCACTCATG GTTATGGCAG 5500 CACTGCATAA TTCTCTTACT GTCATGCCAT CCGTAAGATG CTTTTCTGTG 5550 ACTGGTGAGT ACTCAACCAA GTCATTCTGA GAATAGTGTA TGCGGCGACC 5600 GAGTTGCTCT TGCCCGGCGT CAACACGGGA TAATACCGCG CCACATAGCA 5650 GAACTTTAAA AGTGCTCATC ATTGGAAAAC GTTCTTCGGG GCGAAAACTC 5700 TCAAGGATCT TACCGCTGTT GAGATCCAGT TCGATGTAAC CCACTCGTGC 5750 ACCCAACTGA TCTTCAGCAT CTTTTACTTT CACCAGCGTT TCTGGGTGAG 5800 CAAAAACAGG AAGGCAAAAT GCCGCAAAAA AGGGAATAAG GGCGACACGG 5850 AAATGTTGAA TACTCATACT CTTCCTTTTT CAATATTATT GAAGCATTTA 5900 TCAGGGTTAT TGTCTCATGA GCGGATACAT ATTTGAATGT ATTTAGAAAA 5950 ATAAACAAAT AGGGGTTCCG CGCACATTTC CCCGAAAAGT GCCACCTGAC 6000 GTCTAAGAAA CCATTATTAT CATGACATTA ACCTATAAAA ATAGGCGTAT 6050 CACGAGGCCC TTTCGTCTTC AA 6072

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 237 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe
-23 -10 -10

Ser Ile Ala Thr Asn Ala Tyr Ala Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr 10 Cys Ser Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn Trp Tyr Gln 25 Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Phe Thr Ser Ser Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser 60 Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp 70 75 Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Thr Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala 105 Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser 115 120 Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg 130 135 Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly 150 Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu 175 180 185 Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser 190 195 Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys 205

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 110 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(x:	i) S	EQUE	NCE 1	DESCI	RIPT	ION:	SEQ	ID 1	NO:1	01:				
Asp 1	Ile	Gln	Leu	Thr 5	Gln	Ser	Pro	Ser	Ser 10	Leu	Ser	Ala	Ser	Val 15
Gly	Asp	Arg	Val	Thr 20	Ile	Thr	Cys	Ser	Ala 25	Ser	Gln	Asp	Ile	Ser 30
Asn	Tyr	Leu	Asn	Trp 35	Tyr	Gln	Gln	Lys	Pro 40	Gly	Lys	Ala	Pro	Lys 45
Leu	Leu	Ile	Tyr	Phe 50	Thr	Ser	Ser	Leu	His 55	Ser	Gly	Val	Pro	Ser 60
Arg	Phe	Ser	Gly	Ser 65	Gly	Ser	Gly	Thr	Asp 70	Tyr	Thr	Leu	Thr	Ile 75
Ser	Ser	Leu	Gln	Pro 80	Glu	Asp	Phe	Ala	Thr 85	Tyr	Tyr	Cys	Gln	Gln 90
Tyr	Ser	Thr	Val	Pro 95	Trp	Thr	Phe	Gly	Gln 100	Gly	Thr	Lys	Val	Glu 105
Ile	Lys	Arg	Thr	Val 110										
(2)	INFO	RMAT	ION 1	FOR S	SEQ :	ID NO	0:102	2:						
(:	(1	A) LI B) T	ENGTI YPE :	CHARA H: 11 Amir OGY:	L8 ar	mino cid		ls						
(x:				DESCE			SEO	ו מד	JO : 1 (02:				
							_				Val	Gln	Pro	Gly
1	vai	OIII	Dea	5	Olu	DCI	Oly	Gry	10	Deu	vai	GIII	110	15
Gly	Ser	Leu	Arg	Leu 20	Ser	Cys	Ala	Ala	Ser 25	Gly	Tyr	Thr	Phe	Thr 30
Asn	Tyr	Gly	Met	Asn 35	Trp	Ile	Arg	Gln	Ala 40	Pro	Gly	Lys	Gly	Leu 45
Glu	Trp	Val	Gly	Trp 50	Ile	Asn	Thr	Tyr	Thr 55	Gly	Glu	Pro	Thr	Tyr 60
		_	_,	_	_	_	_,	-1		_		_		_

Ala Ala Asp Phe Lys Arg Arg Phe Thr Ile Ser Ala Asp Thr Ser

65

70

Ser	Asn	Thr	Val	Tyr 80	Leu	Gln	Met	Asn	Ser 85	Leu	Arg	Ala	Glu	Asp 90
Thr	Ala	Val	Tyr	Туг 95	Cys	Ala	Lys	Tyr	Pro 100	His	Tyr	Tyr	Gly	Ser 105
Ser	His	Trp	Tyr	Phe 110	Asp	Val	Trp	Gly	Gln 115	Gly	Thr	Leu		
(2)	INFO	RMAT	ION 1	FOR S	SEQ :	ID NO	0:10	3:						
(:	(1	A) Li B) T	ENGTI YPE :	CHARA H: 1: Amir DGY:	LO ar	mino cid		is						
(x:	i) SI	EQUEI	NCE I	DESCI	RIPT	ON:	SEQ	ID 1	NO:10	03:				
Asp 1	Ile	Gln	Leu	Thr 5	Gln	Ser	Pro	Ser	Ser 10	Leu	Ser	Ala	Ser	Val 15
Gly	Asp	Arg	Val	Thr 20	Ile	Thr	Cys	Ser	Ala 25	Ser	Gln	Asp	Ile	Ser 30
Asn	Tyr	Leu	Asn	Trp 35	Tyr	Gln	Gln	Lys	Pro 40	Gly	Lys	Ala	Pro	Lys 45
Val	Leu	Ile	Tyr	Phe 50	Thr	Ser	Ser	Leu	His 55	Ser	Gly	Val	Pro	Ser 60
Arg	Phe	Ser	Gly	Ser 65	Gly	Ser	Gly	Thr	Asp 70	Tyr	Thr	Leu	Thr	Ile 75
···Ser	Ser	"Leu	-Gln	Pro	-Glu	Asp	"Phe"	Ala	Thr 85	Tyr	Tyr	-Cys	-Gln-	Gln 90
Tyr	Ser	Thr	Val	Pro 95	Trp	Thr	Phe	Gly	Gln 100	Gly	Thr	Lys	Val	Glu 105
Ile	Lys	Arg	Thr	Val 110										
(2)]	NFO	RMAT	ION I	FOR S	SEQ I	D NO	0:104	ł :						
(i	(1	A) LI	ENGTI	CHARA H: 11 Amir	.8 an	nino		ls						

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

(D) TOPOLOGY: Linear

1			Dea	5	Olu	501	<i>327</i>	GIY	10	Dea	vai	O111	FIO	15
Gly	Ser	Leu	Arg	Leu 20	Ser	Cys	Ala	Ala	Ser 25	Gly	Tyr	Thr	Phe	Thr 30
Asn	Tyr	Gly	Met	Asn 35	Trp	Ile	Arg	Gln	Ala 40	Pro	Gly	Lys	Gly	Leu 45
Glu	Trp	Val	Gly	Trp 50	Ile	Asn	Thr	Tyr	Thr 55	Gly	Glu	Pro	Thr	Tyr 60
Ala	Ala	Asp	Phe	Lys 65	Arg	Arg	Phe	Thr	Phe 70	Ser	Ala	Asp	Thr	Ser 75
Ser	Asn	Thr	Val	Tyr 80	Leu	Gln	Met	Asn	Ser 85	Leu	Arg	Ala	Glu	Asp 90
Thr	Ala	Val	Tyr	Tyr 95	Cys	Ala	Lys	Tyr	Pro 100	His	Tyr	Tyr	Gly	Ser 105
Ser	His	Trp	Tyr	Phe 110	Asp	Val	Trp	Gly	Gln 115	Gly	Thr	Leu		
(2)	INFO	TAM	ON I	OR S	SEQ 1	D NO	0:109	5:						
	i) SI (<i>I</i>	EQUEN A) LI B) TY	ION I ICE (ENGTH (PE: DPOL(CHARA I: 11 Amir	ACTER LO an	RISTI nino cid	CS:							
()	i) SI (<i>I</i> (I	EQUEN A) LI B) TY	NCE (ENGTH (PE:	CHARA I: 11 Amir OGY:	ACTER LO am no Ac Line	RISTI mino cid ear	ICS: acid	ls	JO:1()5 :				
i) (xi	i) SI (<i>I</i> (I (I	EQUEN (A) LI (B) TY (C) TO (C) EQUEN	NCE (ENGTH (PE:	CHARA H: 11 Amir OGY:	ACTER 10 am 10 Ac Line	RISTI mino cid car	ICS: acid	is			Ser	Ala	Ser	Val
(xi Asp 1	i) SI (A (I (I i) SI	EQUEN A) LI B) TY C) TO EQUEN	NCE (ENGTH (PE: DPOLO	CHARA H: 11 Amir OGY: DESCR Thr	ACTER 10 am 10 Ac Line RIPTI	RISTI nino cid car [ON:	CS: acid SEQ Pro	ls ID 1 Ser	Ser 10	Leu				15
(xi Asp 1 Gly	i) SI (I (I i) SI Ile	EQUEN A) LI B) TO D) TO EQUEN Gln Arg	NCE (ENGTH (PE: DPOLO NCE I	CHARA H: 11 Amir OGY: DESCR Thr 5 Thr 20	ACTER 10 an 10 Ac Line RIPTI Gln	RISTI mino cid ear ION: Ser	CS: acid SEQ Pro	ID N Ser Ser	Ser 10 Ala 25	Leu [®] Ser	Gln	Asp	Ile	15 Ser 30
(xi Asp 1 Gly Asn	i) SI (I (I (I I I I I I I I I I I I I I I	EQUENCY (A) LEGUEN CONTROL (A) TO	NCE (ENGTH (PE: DPOLC NCE I Leu Val	CHARA I: 11 Amir OGY: DESCR Thr 5 Thr 20 Trp 35	ACTER 10 am no Ac Line RIPTI Gln Ile	RISTIMINO cid car ON: Ser Thr	CCS: acid SEQ Pro Cys	ls ID N Ser Ser Lys	Ser 10 Ala 25 Pro 40	Leu Ser Gly	Gln Lys	Asp Ala	Ile Pro	15 Ser 30 Lys 45
(xi Asp 1 Gly Asn Val	i) SI (I (I i) SI Ile Asp Tyr	EQUENCY LEQUENCY Arg	NCE (ENGTH (PE: DPOLO NCE I Leu Val Asn	CHARA H: 11 Amir OGY: DESCR Thr 5 Thr 20 Trp 35 Phe 50	ACTER 10 and Action of Line RIPTI Gln Ile Tyr	RISTIMINO Cid Car CON: Ser Thr Gln Ser	SEQ Pro Cys Gln Ser	ID N Ser Ser Lys	Ser 10 Ala 25 Pro 40 His 55	Leu Ser Gly Ser	Gln Lys Gly	Asp Ala Val	Ile Pro	15 Ser 30 Lys 45 Ser

				95					100					105
Ile	Lys	Arg	Thr	Val 110										
(2)	INFO	RMAT:	ION I	FOR S	SEQ :	ID N	0:10	5:						
i)	() (I	A) L1	ENGTI YPE :	CHARA H: 1: Amir OGY:	18 ar 10 Ac	mino cid		ls		·				
(xi	i) sı	EQUE	NCE I	DESCI	RIPT:	ON:	SEQ	ID 1	NO:10	06:				
Glu 1	Val	Gln	Leu	Val 5	Glu	Ser	Gly	Gly	Gly 10	Leu	Val	Gln	Pro	Gly 15
Gly	Ser	Leu	Arg	Leu 20	Ser	Cys	Ala	Ala	Ser 25	Gly	Tyr	Thr	Phe	Thr 30
Asn	Tyr	Gly	Met	Asn 35	Trp	Val	Arg	Gln	Ala 40	Pro	Gly	Lys	Gly	Leu 45
Glu	Trp	Val	Gly	Trp 50	Ile	Asn	Thr	Tyr	Thr 55	Gly	Glu	Pro	Thr	Tyr 60
Ala	Ala	Asp	Phe	Lys 65	Arg	Arg	Phe	Thr	Phe 70	Ser	Leu	Asp	Thr	Ser 75
Lys	Ser	Thr	Ala	Tyr 80	Leu	Gln	Met	Asn	Ser 85	Leu	Arg	Ala	Glu	Asp 90
Thr	Ala	Val	Tyr	Tyr 95	Cys	Ala	Lys	Tyr	Pro 100	His	Tyr	Tyr	Gly	Ser 105
Ser	His	Trp	Tyr	Phe 110	Asp	Val	Trp	Gly	Gln 115	Gly	Thr	Leu		
(2)]	NFOF	RMAT:	ION I	FOR S	SEQ I	D NO	0:107	7:						
	(<i>I</i> (E	A) LI 3) T' 0) T(ENGTI PE: OPOLO	CHARA H: 11 Amir OGY:	lO an no Ac Line	mino cid ear	ació		1 0:10)7:				
				Thr 5							Ser	Ala	Ser	Val 15

Tyr Ser Thr Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu

Gly	Asp	Arg	Val	Thr 20	Ile	Thr	Cys	Arg	Ala 25	Asn	Glu	Gln	Leu	Ser 30
Asn	Tyr	Leu	Asn	Trp 35	Tyr	Gln	Gln	Lys	Pro 40	Gly	Lys	Ala	Pro	Lys 45
Val	Leu	Ile	Tyr	Phe 50	Thr	Ser	Ser	Leu	His 55	Ser	Gly	Val	Pro	Ser 60
Arg	Phe	Ser	Gly	Ser 65	Gly	Ser	Gly	Thr	Asp 70	Phe	Thr	Leu	Thr	Ile 75
Ser	Ser	Leu	Gln	Pro 80	Glu	Asp	Phe	Ala	Thr 85	Tyr	Tyr	Cys	Gln	Gln 90
Tyr	Ser	Thr	Val	Pro 95	Trp	Thr	Phe	Gly	Gln 100	Gly	Thr	Lys	Val	Glu 105
Ile	Lys	Arg	Thr	Val 110										
(2)]	INFOR	RMAT	ON I	FOR S	SEQ I	D NO	0:108	3:						
(-	i) SI	ZOLIEN	ICE (זסמשי	ነብጥ አ	פופיים	רכפ י							
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	12	3/ LI	2116711	1. 11	LO ai	IIIIO	aci	15						
	(E	3) T	PE:	Amir	o Ao	cid	acı	15						
(xi	(I	3) TY O) T((PE: OPOLO	Amir OGY:	no Ad Line	cid ear		ID N	JO:10	08:				
	(F (I	B) TY	PE: POLC	Amir OGY: DESCF	no Ao Line RIPTI	cid ear ION:	SEQ				Val	Gln	Pro	Gly 15
Glu 1	(F (I i) SF Val	3) TY D) TO EQUEN	(PE: OPOLO NCE I Leu	Amir OGY: DESCF Val 5	no Ao Line RIPT:	cid ear ION:	SEQ Gly	ID 1	Gly 10	Leu				15
Glu 1 Gly	(I (I i) SE Val Ser	B) TY D) TO EQUEN Gln Leu	(PE: DPOLO NCE I Leu Arg	Amir DGY: DESCF Val 5 Leu 20	no Ac Line RIPTI Glu Ser	eid ear ION: Ser Cys	SEQ Gly Ala	ID N	Gly 10 Ser 25	Leu Gly	Tyr	Thr	Phe	15 Thr 30
Glu 1 Gly Asn	(I (I) SH Val Ser	B) TY D) TO EQUEN Gln Leu Gly	(PE: DPOLC NCE I Leu Arg	Amir DESCF Val 5 Leu 20 Asn 35	DO AC Line RIPTI Glu Ser	eid ear ION: Ser Cys	SEQ Gly Ala Arg	ID N Gly Ala	Gly 10 Ser 25 Ala 40	Leu Gly Pro	Tyr Gly	Thr Lys	Phe Gly	15 Thr 30 Leu 45
Glu 1 Gly Asn Glu	(F (I) SF Val Ser Tyr	Gln Coly C	(PE: DPOLO NCE I Leu Arg Ile	Amir DESCF Val 5 Leu 20 Asn 35 Trp 50	Line RIPT: Glu Ser Trp	eid ear ION: Ser Cys Val	SEQ Gly Ala Arg Thr	ID N Gly Ala Gln	Gly 10 Ser 25 Ala 40 Thr 55	Leu Gly Pro Gly	Tyr Gly Glu	Thr Lys Pro	Phe Gly Thr	Thr 30 Leu 45 Tyr 60
Glu 1 Gly Asn Glu Ala	(F (I) (I) Ser Tyr Trp	Gln Leu Gly Val	(PE: DPOLO NCE I Leu Arg Ile Gly	Amir DGY: DESCF Val 5 Leu 20 Asn 35 Trp 50 Lys 65	CIPTI Glu Ser Trp Ile	eid ear ION: Ser Cys Val Asn	SEQ Gly Ala Arg Thr	ID N Gly Ala Gln Tyr	Gly 10 Ser 25 Ala 40 Thr 55 Phe	Leu Gly Pro Gly Ser	Tyr Gly Glu Leu	Thr Lys Pro Asp	Phe Gly Thr	15 Thr 30 Leu 45 Tyr 60 Ser 75

£1.

Ser	His	Trp	Tyr	Phe 110	Asp	Val	Trp	Gly	Gln 115	Gly	Thr	Leu		
(2)	INFO	RMAT	ION 1	FOR S	SEQ :	ID NO	0:10	9:						
(:	(1	A) L B) T	NCE (ENGTI YPE: OPOL(H: 13 Amir	10 ar	mino cid		ds						
(x:	i) SI	EQUE	NCE I	DESCI	RIPT:	ON:	SEQ	ID 1	10:10	09:				
Asp 1	Ile	Gln	Leu	Thr 5	Gln	Ser	Pro	Ser	Ser 10	Leu	Ser	Ala	Ser	Val 15
Gly	Asp	Arg	Val	Thr 20	Ile	Thr	Cys	Arg	Ala 25	Asn	Glu	Gln	Leu	Ser 30
Asn	Tyr	Leu	Asn	Trp 35	Tyr	Gln	Gln	Lys	Pro 40	Gly	Lys	Ala	Pro	Lys 45
Val	Leu	Ile	Tyr	Phe 50	Thr	Ser	Ser	Leu	His 55	Ser	Gly	Val	Pro	Ser 60
Arg	Phe	Ser	Gly	Ser 65	Gly	Ser	Gly	Thr	Asp 70	Phe	Thr	Leu	Thr	Ile 75
Ser	Ser	Leu	Gln	Pro 80	Glu	Asp	Phe	Ala	Thr 85	Tyr	Tyr	Cys	Gln	Gln 90
Tyr	Ser	Thr	Val	Pro 95	Trp	Thr	Phe	Gly	Gln 100	Gly	Thr	Lys	Val	Glu 105
Ile	Lys	Arg	Thr	Val 110										
(2)	INFO	RMAT	ION I	FOR S	SEQ 1	D NO	:110):						
(:	(<i>I</i>	A) LI 3) T	NCE (ENGTH YPE: OPOL(H: 11 Amir	l8 an	nino cid		ls						
(x:	i) SI	EQUEI	NCE I	ESCF	RIPTI	ON:	SEQ	ID N	10:11	10:				
Glu 1	Val	Gln	Leu	Val 5	Glu	Ser	Gly	Gly	Gly 10	Leu	Val	Gln	Pro	Gly 15

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Asp Phe Thr

20

25

His	Tyr	Gly	Met	Asn 35	Trp	Val	Arg	Gln	Ala 40	Pro	Gly	Lys	Gly	Leu 45
Glu	Trp	Val	Gly	Trp 50	Ile	Asn	Thr	Tyr	Thr 55	Gly	Glu	Pro	Thr	Туг 60
Ala	Ala	Asp	Phe	Lys 65	Arg	Arg	Phe	Thr	Phe 70	Ser	Leu	Asp	Thr	Ser 75
Lys	Ser	Thr	Ala	Tyr 80	Leu	Gln	Met	Asn	Ser 85	Leu	Arg	Ala	Glu	Asp 90
Thr	Ala	Val	Tyr	Tyr 95	Cys	Ala	Lys	Tyr	Pro 100	His	Tyr	Tyr	Gly	Ser 105
Ser	His	Trp	Tyr	Phe 110	Asp	Val	Trp	Gly	Gln 115	Gly	Thr	Leu		
(2)	INFO	TAMS	ION I	FOR S	SEQ :	D NO):11	l:						
(:	(<i>I</i>	A) LI 3) T	NCE (ENGTH YPE: OPOL(H: 11 Amir	LO an	mino cid		is [.]						
(x:	i) SE	EQUE	NCE I	DESCF	RIPTI	ON:	SEQ	ID 1	10:11	.1:				
			NCE I Leu								Ser	Ala	Ser	Val
Asp 1	Ile	Gln		Thr 5	Gln	Ser	Pro	Ser	Ser 10	Leu				15
Asp 1 Gly	Ile Asp	Gln Arg	Leu	Thr 5 Thr 20	Gln	Ser Thr	Pro Cys	Ser Arg	Ser 10 Ala 25	Leu Asn	Glu	Gln	Leu	15 Ser 30
Asp 1 Gly Asn	Ile Asp Tyr	Gln Arg Leu	Leu Val	Thr 5 Thr 20 Trp 35	Gln Ile Tyr	Ser Thr Gln	Pro Cys Gln	Ser Arg Lys	Ser 10 Ala 25 Pro 40	Leu Asn Gly	Glu Lys	Gln Ala	Leu Pro	Ser 30 Lys 45
Asp 1 Gly Asn Val	Ile Asp Tyr Leu	Gln Arg Leu Ile	Leu Val Asn	Thr 5 Thr 20 Trp 35 Phe 50	Gln Ile Tyr Thr	Ser Thr Gln Ser	Pro Cys Gln Ser	Ser Arg Lys Leu	Ser 10 Ala 25 Pro 40 His 55	Leu Asn Gly Ser	Glu Lys Gly	Gln Ala Val	Leu Pro Pro	Ser 30 Lys 45 Ser 60
Asp 1 Gly Asn Val	Ile Asp Tyr Leu Phe	Gln Arg Leu Ile Ser	Leu Val Asn Tyr	Thr 5 Thr 20 Trp 35 Phe 50 Ser 65	Gln Ile Tyr Thr	Ser Thr Gln Ser	Pro Cys Gln Ser	Ser Arg Lys Leu Thr	Ser 10 Ala 25 Pro 40 His 55 Asp	Leu Asn Gly Ser	Glu Lys Gly Thr	Gln Ala Val Leu	Leu Pro Pro Thr	15 Ser 30 Lys 45 Ser 60 Ile
Asp 1 Gly Asn Val Arg	Ile Asp Tyr Leu Phe Ser	Gln Arg Leu Ile Ser Leu	Leu Val Asn Tyr	Thr 5 Thr 20 Trp 35 Phe 50 Ser 65 Pro 80	Gln Ile Tyr Thr Gly	Ser Thr Gln Ser Ser	Pro Cys Gln Ser Gly Phe	Ser Arg Lys Leu Thr	Ser 10 Ala 25 Pro 40 His 55 Asp 70 Thr 85	Leu Asn Gly Ser Phe	Glu Lys Gly Thr	Gln Ala Val Leu Cys	Leu Pro Pro Thr	Ser 30 Lys 45 Ser 60 Ile 75 Gln 90

		(YPE:	H: 1: Amin OGY:	no A	cid	aci	ds						
	(x:	i) S	EQUE	NCE 1	DESCI	RIPT	ION:	SEQ	ID 1	NO:1	12:				
	Glu 1	Val	Gln	Leu	Val 5	Glu	Ser	Gly	Gly	Gly 10	Leu	Val	Gln	Pro	Gly 15
	Gly	Ser	Leu	Arg	Leu 20	Ser	Cys	Ala	Ala	Ser 25	Gly	Tyr	Thr	Phe	Thr 30
	Asn	Tyr	Gly	Ile	Asn 35	Trp	Val	Arg	Gln	Ala 40	Pro	Gly	Lys	Gly	Leu 45
,	Glu	Trp	Val	Gly	Trp 50	Ile	Asn	Thr	Tyr	Thr 55	Gly	Glu	Pro	Thr	Tyr 60
•	Ala	Ala	Asp	Phe	Lys 65	Arg	Arg	Phe	Thr	Phe 70	Ser	Leu	Asp	Thr	Ser 75
•	Lys	Ser	Thr	Ala	Tyr 80	Leu	Gln	Met	Asn	Ser 85	Leu	Arg	Ala	Glu	Asp 90
	Thr	Ala	Val	Tyr	Tyr 95	Cys	Ala	Lys	Tyr	Pro 100	Tyr	Tyr	Tyr	Gly	Thr 105
i	Ser	His	Trp	Tyr	Phe 110	Asp	Val	Trp	Gly	Gln 115	Gly	Thr	Leu		
- (2)]	INFO	RMAT:	ION I	FOR S	SEQ :	ID NO	0:113	3:						
	(1	()	EQUEI A) LI B) T'	ENGTI YPE :	f: 11	LO ar	mino cid		ls						
	(xi	i) s	EQUEI	NCE I	DESCF	RIPT	ON:	SEQ	ID N	10:11	13:				
1	Asp 1	Ile	Gln	Leu	Thr 5	Gln	Ser	Pro	Ser	Ser 10	Leu	Ser	Ala	Ser	Val 15
(Gly	Asp	Arg	Val	Thr 20	Ile	Thr	Cys	Arg	Ala 25	Asn	Glu	Gln	Leu	Ser 30
ž	Asn	Tyr	Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

Val Leu Ile Tyr Phe Thr Ser Ser Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Thr Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu 95 100 Ile Lys Arg Thr Val 110 (2) INFORMATION FOR SEQ ID NO:114: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 118 amino acids (B) TYPE: Amino Acid (D) TOPOLOGY: Linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:114: Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Gln Pro Gly 1 5 Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Asp Phe Thr His Tyr Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr 55 Ala Ala Asp Phe Lys Arg Arg Phe Thr Phe Ser Leu Asp Thr Ser Lys Ser Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp 80 Thr Ala Val Tyr Tyr Cys Ala Lys Tyr Pro Tyr Tyr Tyr Gly Thr 100

, ,

(2) INFORMATION FOR SEQ ID NO:115:

110

Ser His Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Leu

(i) SEQUENCE CHARACTERISTICS:

	•		YPE: OPOL											
(x:	i) S	EQUE	NCE 1	DESC	RIPT	ION:	SEQ	ID 1	NO:1	15:				
Asp 1	Ile	Gln	Leu	Thr 5	Gln	Ser	Pro	Ser	Ser 10	Leu	Ser	Ala	Ser	Val 15
Gly	Asp	Arg	Val	Thr 20	Ile	Thr	Cys	Ser	Ala 25	Ser	Gln	Asp	Ile	Ser 30
Asn	Tyr	Leu	Asn	Trp 35	Tyr	Gln	Gln	Lys	Pro 40	Gly	Lys	Ala	Pro	Lys 45
Val	Leu	Ile	Tyr	Phe 50	Thr	Ser	Ser	Leu	His 55	Ser	Gly	Val	Pro	Ser 60
Arg	Phe	Ser	Gly	Ser 65	Gly	Ser	Gly	Thr	Asp 70	Phe	Thr	Leu	Thr	Ile 75
Ser	Ser	Leu	Gln	Pro 80	Glu	Asp	Phe	Ala	Thr 85	Tyr	Tyr	Cys	Gln	Gln 90
Tyr	Ser	Thr	Val	Pro 95	Trp	Thr	Phe	Gly	Gln 100	Gly	Thr	Lys	Val	Glu 105
Ile	Lys	Arg	Thr	Val 110										
(2)	INFO	RMAT:	ION I	FOR S	SEQ 1	ID NO	0:116	5:						
(:	(<i>1</i>	A) LI 3) T	NCE (ENGTH YPE: OPOL(H: 11 Amir	L8 an	mino cid		ls						
(xi	i) SI	EQUEI	NCE I	DESCI	RIPTI	ON:	SEQ	ID N	10:1 3	L 6 :				
Glu 1	Val	Gln	Leu	Val 5	Glu	Ser	Gly	Gly	Gly 10	Leu	Val	Gln	Pro	Gly 15
Gly	Ser	Leu	Arg	Leu 20	Ser	Cys	Ala	Ala	Ser 25	Gly	Tyr	Asp	Phe	Thr 30
His	Tyr	Gly	Met	Asn 35	Trp	Val	Arg	Gln	Ala 40	Pro	Gly	Lys	Gly	Leu 45
Glu	Trp	Val	Gly	Trp 50	Ile	Asn	Thr	Tyr	Thr 55	Gly	Glu	Pro	Thr	Tyr 60

(A) LENGTH: 110 amino acids

Ala Ala Asp Phe Lys Arg Arg Phe Thr Phe Ser Leu Asp Thr Ser 65 70 75	
Lys Ser Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp 80 85 90	
Thr Ala Val Tyr Tyr Cys Ala Lys Tyr Pro Tyr Tyr Tyr Gly Thr 95 100 105	
Ser His Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Leu 110 115	
(2) INFORMATION FOR SEQ ID NO:117:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 10 amino acids(B) TYPE: Amino Acid(D) TOPOLOGY: Linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:	
Gly Tyr Xaa Xaa Xaa Tyr Gly Xaa Asn 1 5 10	
(2) INFORMATION FOR SEQ ID NO:118:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 17 amino acids(B) TYPE: Amino Acid(D) TOPOLOGY: Linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:	
Trp Ile Asn Thr Xaa Thr Gly Glu Pro Thr Tyr Ala Ala Asp Phe 1 5 10 15	
Lys Arg	
(2) INFORMATION FOR SEQ ID NO:119:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 14 amino acids(B) TYPE: Amino Acid(D) TOPOLOGY: Linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:	
Tyr Pro Xaa Tyr Xaa Xaa Xaa Xaa His Trp Tyr Phe Asp Val	

- (2) INFORMATION FOR SEQ ID NO:120:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
- -(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Xaa Ser Xaa Asp Xaa Xaa Xaa Xaa Thr Xaa 1 5 10

- (2) INFORMATION FOR SEQ ID NO:121:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Xaa Ala Xaa Xaa Xaa Ser Asn Tyr Leu Asn 1 5 10

- (2) INFORMATION FOR SEQ ID NO:122:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Phe Thr Ser Ser Leu His Ser

- (2) INFORMATION FOR SEQ ID NO:123:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Gln Gln Tyr Ser Xaa Xaa Pro Trp Thr 1 5

- (2) INFORMATION FOR SEQ ID NO:124:
 - (i) SEQUENCE CHARACTERISTICS:

	•	D) T		OGY:										
(x	i) Sl	EQUEI	NCE 1	DESCI	RIPT	ION:	SEQ	ID 1	NO:12	24:				
Asp 1	Ile	Gln	Xaa	Thr 5	Gln	Ser	Pro	Ser	Ser 10	Leu	Ser	Ala	Ser	Val 15
Gly	Asp	Arg	Val	Thr 20	Ile	Thr	Cys	Ser	Ala 25	Ser	Gln	Asp	Ile	Ser 30
Asn	Tyr	Leu	Asn	Trp 35	Tyr	Gln	Gln	Lys	Pro 40	Gly	Lys	Ala	Pro	Lys 45
Val	Leu	Ile	Tyr	Phe 50	Thr	Ser	Ser	Leu	His 55	Ser	Gly	Val	Pro	Ser 60
Arg	Phe	Ser	Gly	Ser 65	Gly	Ser	Gly	Thr	Asp 70	Phe	Thr	Leu	Thr	Ile 75
Ser	Ser	Leu	Gln	Pro 80	Glu	Asp	Phe	Ala	Thr 85	Tyr	Tyr	Cys	Gln	Gln 90
Tyr	Ser	Thr	Val	Pro 95	Trp	Thr	Phe	Gly	Gln 100	Gly	Thr	Lys	Val	Glu 105
Ile	Lys	Arg												
(2)	INFO	RMAT:	ION 1	FOR S	SEQ :	ID NO	0:12!	5:						
(:	(1		ENGTI YPE :	H: 12 Amir	23 ar 10 Ac	mino cid		is						
(x:	i) SI	EQUE	NCE I	DESC	RIPT	ON:	SEQ	ID 1	NO:12	25:				
Glu 1	Val	Gln	Leu	Val 5	Glu	Ser	Gly	Gly	Gly 10	Leu	Val	Gln	Pro	Gly 15
Gly	Ser	Leu	Arg	Leu 20	Ser	Cys	Ala	Ala	Ser 25	Gly	Tyr	Xaa	Phe	Thr 30
Xaa	Tyr	Gly	Met	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu

(A) LENGTH: 108 amino acids

(B) TYPE: Amino Acid

35

50

40

55

Glu Trp Val Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr

45

Ala Ala Asp Phe Lys Arg Arg Phe Thr Phe Ser Leu Asp Thr Ser 65 70 75

Lys Ser Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp 80 85 90

Thr Ala Val Tyr Tyr Cys Ala Lys Tyr Pro Xaa Tyr Tyr Gly Xaa 95 100 105

Ser His Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Leu Val Thr
110 115 120

Val Ser Ser

- (2) INFORMATION FOR SEQ ID NO:126:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Gly Tyr Asp Phe Thr His Tyr Gly Met Asn 1 5 10

- (2) INFORMATION FOR SEQ ID NO:127:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Tyr Pro Tyr Tyr Tyr Gly Thr Ser His Trp Tyr Phe Asp Val

- (2) INFORMATION FOR SEQ ID NO:128:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:
- Gly Tyr Xaa Phe Thr Xaa Tyr Gly Met Asn 1 5 10

(2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Tyr Pro Xaa Tyr Tyr Gly Xaa Ser His Trp Tyr Phe Asp Val

(2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 254 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe -23 -15 -10

Ser Ile Ala Thr Asn Ala Tyr Ala Glu Val Gln Leu Val Glu Ser
-5 1 5

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys
10 15 20

Ala Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Met Asn Trp Ile \$25\$ \$30\$ \$35

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Trp Ile Asn
40 45 50

Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Ala Asp Phe Lys Arg Arg
55 60 65

Phe Thr Ile Ser Ala Asp Thr Ser Ser Asn Thr Val Tyr Leu Gln
70 75 80

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala 85 90 95

Lys Tyr Pro His Tyr Tyr Gly Ser Ser His Trp Tyr Phe Asp Val 100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys 115 120 125

Gly	Pro	Ser 130	Val	Phe	Pro	Leu	A1a 135	Pro	Ser	Ser	Lys	Ser 140	Thr	Ser
Gly	Gly	Thr 145	Ala	Ala	Leu	Gly	Cys 150	Leu	Val	Lys	Asp	Tyr 155	Phe	Pro
Glu	Pro	Val 160	Thr	Val	Ser	Trp	Asn 165	Ser	Gly	Ala	Leu	Thr 170	Ser	Gly
Val	His	Thr 175	Phe	Pro	Ala	Val	Leu 180	Gln	Ser	Ser	Gly	Leu 185	Tyr	Ser
Leu	Ser	Ser 190	Val	Val	Thr	Val	Pro 195	Ser	Ser	Ser	Leu	Gly 200	Thr	Gln
Thr	Tyr	Ile 205	Cys	Asn	Val	Asn	His 210	Lys	Pro	Ser	Asn	Thr 215	Lys	Val
Asp	Lys	Lys 220	Val	Glu	Pro	Lys	Ser 225	Cys	Asp	Lys	Thr	His 230	Leu	
(2)]	INFO	TAMS	ON I	FOR S	SEQ :	ID NO	0:131	L:						
	i) SI	EQUE1	ICE (CHAR!	ACTE	RIST	CS:							
	i) SI (<i>I</i>	EQUEN A) LE B) TY	ICE (CHARA I: 15 Amir	ACTEI 58 ar 10 Ac	RISTI mino cid	CS:							
()	i) SI (<i>I</i> (I	EQUEN A) LE B) TY	NCE (ENGTH (PE: OPOL(CHARA I: 15 Amir OGY:	ACTEI 58 ar 10 Ac Line	RISTI mino cid ear	ECS: acio		JO:13	31:				
i) ix)	i) SF (<i>I</i> (I (I	EQUEN A) LE B) TY C) TO	NCE (ENGTH (PE: OPOLO	CHARA H: 19 Amir DGY:	ACTER	RISTI mino cid ear	ECS: acid	ls			Туг	Glu	Lys	Met 15
(xi Ser 1	i) SI (I (I (I i) SI	EQUEN A) LE B) TY C) TO EQUEN	NCE (ENGTH (PE:)POLO ICE I Gly	CHAR/ H: 1! Amir DGY: DESCR Ser 5	ACTEI 58 ar 10 Ac Line RIPTI	RIST: mino cid ear ION:	CS: acio SEQ Gly	ls ID N	Phe 10	Asp	_		_	15
(xi Ser 1 Ala	i) SE (F (I (I i) SE Gly	EQUEN A) LE B) TY D) TO EQUEN Gly	NCE (ENGTH (PE:)POLC NCE I Gly	CHARA H: 19 Amir OGY: DESCH Ser 5 Lys 20	ACTER 58 ar no Ac Line Cly Gly	RIST: mino cid ear ION: Ser Ala	SEQ Gly Met	ls ID N Asp	Phe 10 Glu 25 Leu	Asp Asn	Ala	Asp	Glu	15 Asn 30
(xi Ser 1 Ala	i) SI (I (I (I) SI Gly Asn	EQUEN A) LE B) TO C) TO EQUEN Gly Ala	NCE (ENGTH (PE: DPOLO Gly Asn	CHARA H: 1! Amin DGY: DESCH Ser 5 Lys 20 Asp 35	ACTER 58 ar no Ac Line Gly Gly	RIST: mino cid ear ION: Ser Ala	SEQ Gly Met	ID N Asp Thr	Phe 10 Glu 25 Leu 40	Asp Asn Asp	Ala	Asp Val	Glu Ala	15 Asn 30 Thr 45
(xi Ser 1 Ala Ala	i) SP (P (I (I i) SP Gly Asn Leu	EQUENCY ALA Gly Gly Gly	NCE (PE: OPOLO NCE I Gly Asn Ser	CHARA H: 19 Amir OGY: DESCR Ser 5 Lys 20 Asp 35 Ala 50	ACTER 58 ar 10 Ac Line RIPTI Gly Gly Ala	RIST: mino cid ear ION: Ser Ala Lys Asp	SEQ Gly Met	ID N Asp Thr	Phe 10 Glu 25 Leu 40 Ile 55	Asp Asp Gly	Ala Ser Asp	Asp Val Val	Glu Ala Ser	15 Asn 30 Thr 45 Gly 60

100

105

Asn Asn Phe Arg Gln Tyr Leu Pro Ser Leu Pro Gln Ser Val Glu

Cys Arg Pro Phe Val Phe Ser Ala Gly Lys Pro Tyr Glu Phe Ser
110 115 120

Ile Asp Cys Asp Lys Ile Asn Leu Phe Arg Gly Val Phe Ala Phe 125 130 135

Leu Leu Tyr Val Ala Thr Phe Met Tyr Val Phe Ser Thr Phe Ala 140 -145 150

Asn Ile Leu Arg Asn Lys Glu Ser 155